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<130> 2314-241

<151> 2000-07-21

<151> 2001-02-05

<160> 413

<170> PatentIn version 3.0

 $\langle 210 \rangle$  1

<211> 318

<212> DNA

<213>	Unknown
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 $\langle 220 \rangle$ 

<223> unknown *Conus* species

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aattttctcca cgttgactcg tcgctgcctt tctcccggaat cacgatgtca taagacaatg 180

cgtaactgct gcacttcacg ctcttcatac aaagggaaat gtcggcctcg aaaatgaacc 240

actcatcacc tactcctctg gaggcctcag aggaattaca ttgaaataaa agccgcatta 300

Caaaaaaaaa aaaaaaaaaa 318

 $\langle 210 \rangle \quad 2$ 

<211> 76

<212> PRT

<213> Unknown

 $\langle 220 \rangle$ 

<223> unknown *Conus* species

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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His  
20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu  
35 40 45

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys  
35 40 45

Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro  
35 40 45

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly

35 40 45  
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 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly  
 65 70

<210> 12  
 <211> 28  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 12  
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 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

<210> 13  
 <211> 323  
 <212> DNA  
 <213> Conus arenatus

<400> 13  
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 actaggcagt gctcggctaa cggtggatct tgtactogtc attttcaactg ctgcagcctc 180  
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 caataaaaaa aaaaaaaaaa aaa 323

<210> 14  
 <211> 73  
 <212> PRT  
 <213> Conus arenatus

<400> 14  
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 1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
 35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
 50 55 60

091003 07301

Ser Val Cys Val Ala Thr Ser Tyr Pro  
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<210> 15  
<211> 33  
<212> PRT  
<213> Conus arenatus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gn or pyro-Glu; Xaa at residue 33 is Pro or H  
yp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 15  
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

<210> 16  
<211> 326  
<212> DNA  
<213> Conus arenatus

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ctgagggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat 180  
tgtacttttg atcgacactg ctgcagcggc tactgccata aaacaatcca ggcattgttca 240  
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ctgcattgaa ataaaagccg cattgc 326

<210> 17  
<211> 74  
<212> PRT  
<213> Conus arenatus

<400> 17  
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1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His  
20 25 30

His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys  
35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly  
50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
65 70

00910031-0300T660

<210> 18  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is  
 Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

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 1 5 10 15  
 Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 19  
 <211> 332  
 <212> DNA  
 <213> Conus arenatus

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 ctgaggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cggtggatct 180  
 tgttctcgtc attttcaactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240  
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<210> 20  
 <211> 79  
 <212> PRT  
 <213> Conus arenatus

<400> 20  
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 1 5 10 15  
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 20 25 30  
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
 35 40 45  
 Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
 50 55 60  
 Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro  
 65 70 75

<210> 21  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE

00010082-02304  
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25

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<220>
<221> misc_feature
<222> (1)..(345)
<223> n may be any nuclideotide
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<210>	29
<211>	74
<212>	PRT
<213>	Conus arenatus

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<210> 30
<211> 28
<212> PRT
<213> Conus arenatus
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<400>   30
Thr  Cys  Asn  Thr  Xaa  Thr  Xaa  Xaa  Cys  Thr  Leu  His  Gln  His  Cys  Cys
 1                               10                               15

Ser  Gly  His  Cys  His  Lys  Thr  Ile  Gln  Ala  Cys  Ala
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<210> 31  
 <211> 322  
 <212> DNA  
 <213> Conus arenatus

<400> 31  
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 actaggcagt gctcgcctat cgggtggatat tgtactcttc atattcactg ctgcagcaac 180  
 cattgcatta aacctatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac 240  
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<210> 32  
 <211> 70  
 <212> PRT  
 <213> Conus arenatus

<400> 32  
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 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30  
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr  
 35 40 45  
 Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile  
 50 55 60  
 Gly Arg Cys Val Ala Thr  
 65 70

<210> 33  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 33  
 Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr  
 20 25 30

<210> 34  
 <211> 318  
 <212> DNA  
 <213> Conus arenatus

<400> 34  
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ctcactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120  
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 cattgcatta aacctatcga ccgatgtgtg gcaacctgat acccgggcgt ggtcatgaac 240  
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300  
 caaaaaaaaa aaaaaaaaaa 318

<210> 35  
 <211> 70  
 <212> PRT  
 <213> Conus arenatus

<400> 35  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30  
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr  
 35 40 45  
 Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile  
 50 55 60  
 Asp Arg Cys Val Ala Thr  
 65 70

<210> 36  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 36  
 Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr  
 20 25 30

<210> 37  
 <211> 374  
 <212> DNA  
 <213> Conus aurisiacus

<400> 37  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
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 tccatgtcga ctgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc 180  
 tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgata ttcccccttc 240

<400>	40								
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acagctgatg	actccagagg	tacgcagaag	catcgttccc	tgaggctogaa	gaccaaactc				120
tccatgtcga	ctggctgcat	ggaagccgga	tcttattgcg	gctctactac	gagaatctgc				180
tgcggttttt	gcgcttattt	cggcaaaaaa	tgtattgact	atcccagcaa	ctgatcttcc				240
ccctactgtg	ctctatcctt	ttctgcttga	gtcctcctta	cctgagagtg	gtcatgaacc				300
actcatcacc	tgctcctctg	gaggccccag	aggagctaca	ttgaaataaa	atcgcattgc				360
taaaaaaaaa	aaaaaaaaaa								380

<210> 41  
 <211> 77  
 <212> PRT  
 <213> Conus aurisiacus

<400> 41  
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 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu  
 35 40 45  
 Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys  
 50 55 60  
 Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
 65 70 75

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 is Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 42  
 Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys  
 1 5 10 15  
 Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn  
 20 25 30

<210> 43  
 <211> 373  
 <212> DNA  
 <213> Conus aurisiacus

<400> 43  
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 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120  
 agctcggcca ccaaactctc catgtcgact cgctgcaagg cttaaaggaaa accatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgtgg ctgatccagt 240  
 gctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct tacctgagag 300  
 tggatcatgaa cactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata 360  
 aaagccgcat tgc 373

<210> 44  
 <211> 71  
 <212> PRT  
 <213> Conus aurisiacus

&lt;400&gt; 44

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala  
 35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

&lt;210&gt; 45

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(25)

&lt;223&gt; Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 45

Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

&lt;210&gt; 46

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 46

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acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgcccgt 120

aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180

ggatttgaca acgactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg 240

atccagegcc tgatcttccc ctttctgtgc tctatccttt tctgcccagag tcttccttac 300

ctgagagtgg tcatgaacca ctcatcacct gctccctgga ggccctcagag gagctacaat 360

gaaataaaag ccgcattgc 379

&lt;210&gt; 47

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 47

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

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Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
50 55 60

Asp Pro Gly Arg Asn Ile Cys Thr  
65 70

<210> 48  
<211> 26  
<212> PRT  
<213> Conus aurisiacus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 48  
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr  
20 25

<210> 49  
<211> 382  
<212> DNA  
<213> Conus bullatus

<400> 49  
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aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgcgga 180  
cctgctacta cgaaaatctg ctgcgatttt tgcagtcctat tcagcgatag atgtatgaac 240  
aatcccaaca attgatcttc ccccttgtgt gctccatcct tttctgctg agtcctcctt 300  
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360  
attgaaataa aagccgcatt gc 382

<210> 50  
<211> 78  
<212> PRT  
<213> Conus bullatus

<400> 50  
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe

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50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn  
65 70 75

<210> 51  
<211> 36  
<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE  
<222> (1)..(36)  
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,  
25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono  
-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 51  
Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr  
1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn  
20 25 30

Asn Xaa Asn Asn  
35

<210> 52  
<211> 400  
<212> DNA  
<213> Conus bullatus

<400> 52  
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acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120  
aggaaggcca ccaaacaccc tgtgtcgact cgctgcatta ctccaggaac acgatgtaag 180  
gttccgagcc aatgctgcag aggtccttgc aagaacggtc gttgtactcc atccccttct 240  
gaatggtaaa tgtggttgat ccagcgctg atcttcccc ttcgtcgtgc tccatccttt 300  
tctgcctgag tctccttac ctgagagtgg tcatgaacca ctcatcacct actcccctgg 360  
aggcttcaga ggagctacat tgaaataaaa gccgcattgc 400

<210> 53  
<211> 76  
<212> PRT  
<213> Conus bullatus

<400> 53  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys His Pro Val Ser Thr Arg Cys Ile Thr  
35 40 45

Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Gly Pro Cys  
50 55 60

0950003-0304  
T06020-2800T660

Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
65 70 75

<210> 54  
<211> 31  
<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa at residue 4,  
11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo  
Tr

<400> 54  
Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg  
1 5 10 15

Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa  
20 25 30

<210> 55  
<211> 379  
<212> DNA  
<213> Conus bullatus

<400> 55  
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acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgcccctg 120  
aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt 180  
ggatttcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgtagctg 240  
atccggcgctc ttgatcctcc gcttctgtgc tccatctttt ctgcctgagt cctccttacc 300  
tgagagtggc catgaaccac tcatcaccta ctctcttgga ggcttttagag gagctacatt 360  
gaaataaaaag ccgcattgc 379

<210> 56  
<211> 72  
<212> PRT  
<213> Conus bullatus

<400> 56  
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Arg Thr Cys Thr  
65 70

<210> 57  
<211> 26

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<212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57  
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr  
 20 25

<210> 58  
 <211> 373  
 <212> DNA  
 <213> Conus bullatus

<400> 58  
 accaaaacca tcataaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120  
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 180  
 aggattgogt ataactgctg caagtattct tgcagaaatg gtaaattgtg ctgatccagc 240  
 gcctgatctt ccccttctgt tgctccatcc ttttctgcct ggtcctcct tacctgagag 300  
 tggatcatgaa ccaactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360  
 aaagccgcat tgc 373

<210> 59  
 <211> 71  
 <212> PRT  
 <213> Conus bullatus

<400> 59  
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly  
 35 40 45

Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser  
 50 55 60

Cys Arg Asn Gly Lys Cys Gly  
 65 70

<210> 60  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE

09910082-073301

<222> (1)..(25)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 60

Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15

Lys Xaa Ser Cys Arg Asn Gly Lys Cys  
20 25

<210> 61

<211> 382

<212> DNA

<213> Conus bullatus

<400> 61

atcaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120  
aagtgcacct ccaaagtctc caagtgcact agctgcatgg cagccggatc ttattgcgga 180  
cctgctacta cgaatatctg ctgcgatttt tgcagtcctc tcagcgatag atgtatgaaa 240  
aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt 300  
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360  
attgaaataa aagccgcatt gc 382

<210> 62

<211> 78

<212> PRT

<213> Conus bullatus

<400> 62

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala  
35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe  
50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn  
65 70 75

<210> 63

<211> 36

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

0910082 07301  
T06240 2800760

Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr  
1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys  
20 25 30

Lys Xaa Asn Asn  
35

<213> Conus bullatus

accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcattat agctgaggac tccagaggta cgcagttgca tcgtgccctg 120

aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180

aggacttcgt atgactgctg cacgggttct tgcagaaatg gtagatgtgg ctgatccagc 240

gcctgatctt cccctttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300

tggatcatgaa ccactcatca cctactcttc tggaggcttc agaggagcta cattgaaata 360

aaagccgcat tgc 373

<213> Conus bullatus

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser  
35 40 45

Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
50 55 60

Cys Arg Asn Gly Arg Cys Gly  
65 70

<213> Conus bullatus

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys  
20 25

<210> 67  
<211> 321  
<212> DNA  
<213> Conus characteristicus

<400> 67  
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggcctgtcaa 60  
ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120  
actaggcagt gctcggctaa cgggtggatct tgtactcgtc attttcaactg ctgcagcctc 180  
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240  
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300  
caaaaaaaaa aaaaaaaaaa a 321

<210> 68  
<211> 73  
<212> PRT  
<213> Conus characteristicus

<400> 68  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
20 25 30  
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
35 40 45  
Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
50 55 60  
Ser Val Cys Val Ala Thr Ser Tyr Pro  
65 70

<210> 69  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 69  
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15  
Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

09910067-07301

<210> 70  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<400> 70  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly  
 20 25

<210> 71  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
 -sulpho-Tyr or O-phospho-Ty

<400> 71  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Arg Cys  
 20 25

<210> 72  
 <211> 229  
 <212> DNA  
 <213> Conus catus

<400> 72  
 tcgactcgct gccagggtag aggagcatca tgtcgtaaga ctatgtataa ctgctgcagc 60  
 gggtcttgca acagaggtag ttgtggctga tccggcgct gatcttcccc cttccgtgct 120  
 ctatcctttt ctgcctgatt cctccttacc tgagagcggc catgaaccac tcatcacctg 180  
 ctcctctgga ggctcagag gagctacatt gaaataaaaag ccgcattgc 229

<210> 73  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 73  
 Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr  
 1 5 10 15  
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly  
 20 25

<210> 74  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O

-sulpho-Tyr or O-phospho-Ty

<400> 74

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
20 25

<210> 75

<211> 235

<212> DNA

<213> Conus catus

<400> 75

tcgacacgct gcttgccctgc cggagagtct tgccttttta gtaggattag atgctgcggt 60

aactgcagtt cagtcttaaa gtcattgtgtg agctgatcca gctgctgac ttctctctcc 120

tgtgctccat ccttttctgc ctgagtcctc cttatctgag agtggatcatg aaccactcac 180

cacctactct tctggaggct tcagaggagc tacagtgaat taaaagccgc attgc 235

<210> 76

<211> 31

<212> PRT

<213> Conus catus

<400> 76

Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile  
1 5 10 15

Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25 30

<210> 77

<211> 28

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 3 is  
Pro or Hy

<400> 77

Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25

<210> 78

<211> 227

<212> DNA

<213> Conus catus

<400> 78

tcgacacgct gccaggtag aggaggacca tgtactaagg ctgtgtttta ctgctgcagc 60

ggttcttgca acagaggtag atgtggctga tccagcgcct gatcttcccc cttctgtgct 120

ctatcctttt ctgcctgagt cctccttact gagagtagtc atgaaccact catcacctac 180

0910082-073301



tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc

227

<210> 79  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 79  
 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe  
 1 5 10 15  
 Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
 20 25

<210> 80  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp

<400> 80  
 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 81  
 <211> 236  
 <212> DNA  
 <213> Conus catus

<400> 81  
 ttaactttgc gctgcgcaac ttacggaaaa ccttggtgta ttcaaaacga ctgctgcaat 60  
 acatgcatc cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccctt 120  
 ctgtgctcta tccttttctg cctgagtcct ccttacctga gagtgggtcat gaaccactca 180  
 tcacctgctc ctctggaggc ctcgggggag ctacattgaa ataaaagccg cattgc 236

<210> 82  
 <211> 30  
 <212> PRT  
 <213> Conus catus

<400> 82  
 Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn  
 1 5 10 15  
 Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
 20 25 30

<210> 83  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 83

Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 84

<211> 229

<212> DNA

<213> Conus catus

<400> 84

tcgactcgct gccggggtag aggaggacca tgtactaagg ctatgtttaa ctgctgcagc 60

ggttcttgca acagaggttag atgtggctga tccagcgctt gatcttcccc cttctgtgct 120

ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta 180

ctcctctgga ggctcagag aagcatcatt gaaataaaaag ccgcattgc 229

<210> 85

<211> 29

<212> PRT

<213> Conus catus

<400> 85

Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe  
1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
20 25

<210> 86

<211> 25

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp

<400> 86

Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 87

<211> 374

<212> DNA

<213> Conus circumcisis

<400> 87

accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctoctg 60

acgacctgtc aactcatcac agctgatgac tccagaggtg cgcaggagca tcgtgcctctg 120

09910083-072001

aggctcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180  
 aagactatgt ataactgctg cagcggttct tgcagcaacg gtagatgtgg ctgatccagc 240  
 gcctgatctt cccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga 300  
 gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360  
 aaaagccgca ttgc 374

<210> 88  
 <211> 71  
 <212> PRT  
 <213> Conus circumciscus

<400> 88  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30  
 Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly  
 35 40 45  
 Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser  
 50 55 60  
 Cys Ser Asn Gly Arg Cys Gly  
 65 70

<210> 89  
 <211> 25  
 <212> PRT  
 <213> Conus circumciscus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 89  
 Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Ser Asn Gly Arg Cys  
 20 25

<210> 90  
 <211> 379  
 <212> DNA  
 <213> Conus circumciscus

<400> 90  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggctcggcca ccaaagtctc caagtgcgact agctgcatgg aagccggatc ttattgccgc 180  
 tctactacga gaacctgctg cggttattgc tcttatttca gcaaaaaatg tattgacttt 240  
 cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctgagt cctccttacc 300

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<210> 91
<211> 77
<212> PRT
<213> Conus circumcissus
```

```
<210> 92
<211> 35
<212> PRT
<213> Conus circumcissus
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```

<400> 92
Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
1 5 10 15
Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe
20 25 30

```

```
<210> 93
<211> 379
<212> DNA
<213> Conus circumcissus
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<400>	93						
accaaaaccca	tcatcaaaat	gaaactgacg	tgtgtggtga	togtcgcoct	gctgctcctg		60
acgacctgtc	aactcatcac	agctgatgac	tccagaggta	cgcaggagca	togtcocctg		120
aggtcggaca	ccaaactccc	catgtogact	cgctgcaaga	gtaaaggagc	aaaatgttca		180
aggcttatgt	atgactgctg	cagcggttct	tgcagcaggt	actcaggtag	atgtggctga		240
tccagocgct	gatcttcccc	cttctgctgc	tctatccttt	tctgocctgag	tcctccttac		300
ctgagagtgg	tcatgaacca	ctcatcacct	actcctctgg	aggcccagag	gagctacatt		360

379

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<400>      94
Met  Lys  Leu  Thr   Cys  Val  Val  Ile  Val  Ala  Val  Leu  Leu  Leu  Thr  Thr
 1                               5                10                15

Cys  Gln  Leu  Ile   Thr  Ala  Asp  Asp   Ser  Arg  Gly  Thr  Gln  Glu  His  Arg
                20                25                30

Ala  Leu  Arg   Ser  Asp  Thr  Lys  Leu  Pro  Met  Ser  Thr  Arg  Cys  Lys  Ser
          35                40                45

Lys  Gly  Ala  Lys  Cys  Ser  Arg  Leu  Met  Tyr  Asp  Cys  Cys  Ser  Gly  Ser
      50                55                60

Cys  Ser  Arg  Tyr  Ser  Gly  Arg  Cys  Gly
65                70

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<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-
      Tyr, O-sulpho-Tyr or O-phospho-Ty
```

```
<210> 96
<211> 379
<212> DNA
<213> Conus circumciscus
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<400>	96						
acccaaaccca	tcatcaaaat	gaaactgacg	tgtgtggtga	togtcgccgt	gctgctcctg		60
acgacctgtc	aactcatcac	agctgatgac	tccagaggta	cgcagaagca	tcgttccctg		120
acgtcggcca	ccaaagtctc	caagtcgact	ggctgcatga	aagccggatc	ttattgccgc		180
tctactacga	gaacttgctg	cggttattgc	gcttatttgc	gcaaaaaatg	tattgactat		240
cccagcaact	gatcttcccc	ctactgtgct	ctatcctttt	ctgcctaagt	cctccttacc		300
tgagagtggc	catgaaccac	tcatcaccc	actcctctgg	aggcccagag	gagctacatt		360
gaaataaaaq	ccgcattgc						379

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<210> 97
<211> 77
<212> PRT
<213> Conus circumciscus
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<400> 98
Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
1      5      10      15
Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
20      25      30
Xaa Ser Asn
35

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[illegible]

<400> 100

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
65 70

<210> 101

<211> 26

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 101

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 102

<211> 237

<212> DNA

<213> Conus consors

<400> 102

atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc 60

acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120

tccatgtcga ctcgctgcaa gggtagcagga aaacatgca gtaggattgc gtataactgc 180

tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca ggcctgatc tcccccc 237

<210> 103

<211> 71

<212> PRT

<213> Conus consors

<400> 103

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
50 55 60

0991003-03301

Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 104  
<211> 25  
<212> PRT  
<213> Conus consors

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 104  
Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 105  
<211> 320  
<212> DNA  
<213> Conus consors

<400> 105  
atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60  
acagctgatg actccaaagg tacgcagaag catcggtccc tgaggtcgac caccaaagtc 120  
tccaaggcga ctgactgcat tgaagccgga aattattgcg gacctactgt tatgaaaatc 180  
tgctgcgggt tttgcagtcc atacagcaaa atatgtatga actatcccca aaattgatct 240  
tcccccttct gtgctctatc cttttctgcc tgagtcctcc ttacctgaga gtggatcatga 300  
accactcatc acctcgtccc 320

<210> 106  
<211> 78  
<212> PRT  
<213> Conus consors

<400> 106  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg  
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu  
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe  
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn  
65 70 75

<210> 107  
<211> 36  
<212> PRT  
<213> Conus consors

09910083.07301



<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 107  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn  
 20 25 30

Xaa Xaa Gln Asn  
 35

<210> 108  
 <211> 321  
 <212> DNA  
 <213> Conus consors

<400> 108  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60  
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120  
 tccatgtcga ctgcgtgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc 180  
 tgccacggtt cttgcagcag cagcaagggg agatgtggct gatccggcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtctctctta cctgagaggt ggtcatgaac 300  
 cactcatcac ctgctccct g 321

<210> 109  
 <211> 73  
 <212> PRT  
 <213> Conus consors

<400> 109  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser  
 50 55 60

Cys Ser Ser Ser Lys Gly Arg Cys Gly  
 65 70

<210> 110  
 <211> 27  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE

09010082 072301

<222> (1)..(27)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 110

Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys  
1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
20 25

<210> 111

<211> 292

<212> DNA

<213> Conus consors

<400> 111

ggatccatga aactgaogtg catggtgacg gtcgccgtgc tgctcctgac ggctgtgcaa 60  
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120  
aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180  
gactgctgca ccggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240  
cccttctgtg ctctatcctt ttctgctga gtcattcata cctgtgctcg ag 292

<210> 112

<211> 71

<212> PRT

<213> Conus consors

<400> 112

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
50 55 60

Cys Asn Arg Gly Lys Cys Gly  
65 70

<210> 113

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 113

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
20 25

0910083-07301

<210> 114  
 <211> 299  
 <212> DNA  
 <213> Conus consors

<400> 114  
 ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgaa gtcggacacc 120  
 aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac 180  
 gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240  
 atcttcccc tctgtgtctc tctcttttc tgcctgagtc atccatacct gtgctcgag 299

<210> 115  
 <211> 72  
 <212> PRT  
 <213> Conus consors

<400> 115  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45  
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
 50 55 60  
 Asp Pro Ala Arg Lys Thr Cys Thr  
 65 70

<210> 116  
 <211> 26  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 116  
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 117  
 <211> 434  
 <212> DNA  
 <213> Conus consors

<220>  
 <221> misc\_feature

<222> (1)..(434)

<223> n may be any nucleotide

<400> 117

```

ggatccatga aactgacgtg tgtgggtgatc gtcgccgtgc tgctcctgac ggccctgtcaa      60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc      120
aaactctcca tgtcgactcg ctgcaagggc acaggaaaac catgcagtag ggttgcgatat      180
aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc      240
cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc      300
actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg      360
cantgnanaa aannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnggaaaaaa      420
aaaaaaaaaa aaaa                                                    434

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<210> 118

<211> 71

<212> PRT

<213> Conus consors

<400> 118

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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
          35          40          45
Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
          50          55          60
Cys Arg Ser Gly Lys Cys Gly
65          70

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<210> 119

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 119

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Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
1          5          10          15

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Thr Gly Ser Cys Arg Ser Gly Lys Cys
          20          25

```

<210> 120

<211> 393

<212> DNA

<213> Conus consors

<400> 120

09910088-012301660

ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctoctgac ggcctgtcaa 60  
 ctcacacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc 120  
 aaagtctcca agtcgactag ctgcatgaaa gccgggtott attgccgctc tactacgaga 180  
 acctgctgcg gttattgcgc ttatttcggc aaattttgta ttgactttcc cagcaactga 240  
 tcttccccct actgtgctct atccttttct gcctctgcct gagtcctcct tacctgagag 300  
 tggatcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata 360  
 aaagccgcat tgcaaaaaaa aaaaaaaaaa aaa 393

<210> 121  
 <211> 77  
 <212> PRT  
 <213> Conus consors

<400> 121  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45  
 Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
 50 55 60  
 Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn  
 65 70 75

<210> 122  
 <211> 35  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
 pho-Ty

<400> 122  
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
 1 5 10 15  
 Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe  
 20 25 30  
 Xaa Ser Asn  
 35

<210> 123  
 <211> 361  
 <212> DNA  
 <213> Conus dalli

<400> 123  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttctg 60

acggcctgtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg 120  
 aggtcgacca tcaaacactc catgttgact aggagctgca cgctcccgg aggaccttgt 180  
 gggtattata atgactgctg cagtcacaa tgcaatataa gcagaaataa atgcgagtag 240  
 ctgatccggc atctgatctt ccccttctgt gctcgtccta acctgagagt ggatcatgaac 300  
 catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360  
 c 361

<210> 124  
 <211> 73  
 <212> PRT  
 <213> Conus dalli

<400> 124  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr  
 35 40 45  
 Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60  
 Cys Asn Ile Ser Arg Asn Lys Cys Glu  
 65 70

<210> 125  
 <211> 28  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4,  
 5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 125  
 Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa  
 20 25

<210> 126  
 <211> 350  
 <212> DNA  
 <213> Conus distans

<400> 126  
 accaaaacca tcatacaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttctctg 60  
 acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa 120  
 acctccgggt caacgaagag atgcgaagat cctgggtgaac cttgcggaag tgatcattcc 180  
 tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctgggtctgg catctgacca 240

ttcccccttct gtactctatc tctattgcct gagtcatctt tacctgtgag tggatcatgaa 300  
tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350

<210> 127  
<211> 66  
<212> PRT  
<213> Conus distans

<400> 127  
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser  
20 25 30  
Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro  
35 40 45  
Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val  
50 55 60

Cys Ala  
65

<210> 128  
<211> 25  
<212> PRT  
<213> Conus distans

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 7 is Pro or Hy

<400> 128  
Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly  
1 5 10 15  
Gly Ser Cys Asn His Asn Val Cys Ala  
20 25

<210> 129  
<211> 309  
<212> DNA  
<213> Conus ermineus

<400> 129  
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
acagctgacg actccagacg tacgcagaag catcgtgccc tgaggctgac caccaaacgc 120  
gccacgtcga atcgccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180  
tgctgcaata aaacgtgcac cagatcaaaa tgccctgat cttccccctt ctgtgctgta 240  
tccttttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc 300  
ctctggagg 309

<210> 130  
<211> 72  
<212> PRT

091033-0730T660





Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val  
 35 40 45

Ser Lys Ser Lys Cys Asn  
 50

<210> 134

<211> 27

<212> PRT

<213> Conus ermineus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Tr

<400> 134

Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 135

<211> 385

<212> DNA

<213> Conus geographus

<400> 135

ggatccatga aactgacgtg cgtggtgata gtcgccgtgc tgctcctgac ggccctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctggg gtcgaccacc 120  
 gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180  
 aattgctgca ggtcttgcaa tccatacgcc aaaagatggt acggctaata cagcgctga 240  
 tcttccccct tctgtgctct atcccttctt gtctgagtc tcttacctg agagtgggtca 300  
 tgaaccactc ctcacctaact tctctggagg cttcggagga gctacattga aataaaagcc 360  
 gcattgtaaa aaaaaaaaaa aaaaa 385

<210> 136

<211> 73

<212> PRT

<213> Conus geographus

<400> 136

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Ala Lys Arg Cys Tyr Gly  
 65 70

0910083.07301  
 T02240"2800T660

<210> 137  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22  
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Ty

<400> 137  
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15  
 Arg Ser Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa  
 20 25

<210> 138  
 <211> 396  
 <212> DNA  
 <213> Conus geographus

<400> 138  
 ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggctgtgcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcgtccacc 120  
 aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt 180  
 gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgctacta acccagcgcc 240  
 tgatcttccc ccttctgtgc tctattcctt tctgcctgag tcctccttac ctgaaagtgg 300  
 tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa 360  
 gccgcattgc aatgacaaaa aaaaaaaaaa aaaaaa 396

<210> 139  
 <211> 74  
 <212> PRT  
 <213> Conus geographus

<400> 139  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser  
 35 40 45  
 Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys  
 50 55 60  
 Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr  
 65 70

<210> 140  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

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<220>
<221>  PEPTIDE
<222>  (1)..(27)
<223>  Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
      and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr

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or O-phospho-Ty

<400> 143

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa  
20 25

<210> 144

<211> 28

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 144

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly  
20 25

<210> 145

<211> 26

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 145

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys  
20 25

<210> 146

<211> 314

<212> DNA

<213> Conus geographus

<400> 146

catcacagct gatgactcca gaggtacgca gaagcatcgt gccctgaggt cgtccaccaa	60
actcaccttg tcgactcgct gcaaatacacc cggaactcca tgttcaaggg gtatgctga	120
ttgctgcacg tcttgcttggt tatacagcaa caaatgtagg cgctactaac ccagcgctg	180
atcttccccc ttctgtgctc tattcctttc tgctgagtc ctcttacct gaaagtggtc	240
atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc	300
cgcattgcaa tgac	314

<210> 147  
 <211> 55  
 <212> PRT  
 <213> Conus geographus

<400> 147  
 Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg  
 1 5 10 15  
 Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr  
 20 25 30  
 Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr  
 35 40 45  
 Ser Asn Lys Cys Arg Arg Tyr  
 50 55

<210> 148  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 148  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 149  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 149  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 150  
 <211> 380  
 <212> DNA  
 <213> Conus laterculatus

<400> 150  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac cgctgatgac tccagaggta cgcagaagca tcgtgcctg 120

09910082-0730

<210>	151
<211>	72
<212>	PRT
<213>	Conus laterculatus

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<210> 152
<211> 27
<212> PRT
<213> Conus laterculatus
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<400> 152
Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
1 5 10 15
Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa
20 25
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<400> 153
accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg      60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg      120
aggtcgacca ccaaactctc catatcgact cgctgccttc ctcccggaac atattgtaag      180
gcgacaacgg aagtctgctg ctcttcttgc cttcaattcg ctcagatatg ttcggggttga      240

```

tcttccctct tctgtgctct atccttttct gectgagtcc tccatacctg agaatggcca 300  
tgaaccactc aacatctact cctctggagg cctcagaaga gctatatattga aataaaagcc 360  
gcattgc 367

<210> 154  
<211> 73  
<212> PRT  
<213> Conus laterculatus

<400> 154  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30  
Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro  
35 40 45  
Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys  
50 55 60  
Leu Gln Phe Ala Gln Ile Cys Ser Gly  
65 70

<210> 155  
<211> 27  
<212> PRT  
<213> Conus laterculatus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 4 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 155  
Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys  
1 5 10 15  
Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser  
20 25

<210> 156  
<211> 373  
<212> DNA  
<213> Conus laterculatus

<400> 156  
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccgatc atcatgtagc 180  
gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240  
ggctgaactt ccccttctg tgctctatcc ttttotgcc gagtctcca tacctgagag 300  
tggtcatgaa ccaactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360  
aaagccgcat tgc 373

09910082-072301

<210> 157  
 <211> 75  
 <212> PRT  
 <213> Conus laterculatus

<400> 157  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser  
 35 40 45  
 Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys  
 50 55 60  
 Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly  
 65 70 75

<210> 158  
 <211> 29  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 3 is Pro or Hyp

<400> 158  
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys  
 1 5 10 15  
 Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg  
 20 25

<210> 159  
 <211> 330  
 <212> DNA  
 <213> Conus laterculatus

<400> 159  
 accaaaacac tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcgacaa ccaaactctc catgctgact cggacctgct ggccttccgg aacagcttgt 180  
 ggtattgata gtaactgctg cagtggatgc aatgtatcca gaagtaaag taactagctg 240  
 attcggcgctc taaacttcct ccttctgcct gagtcctcca tacctgagag tggatcatgaa 300  
 ccacatcatc acctcatctc tggaggcctc 330

<210> 160  
 <211> 72  
 <212> PRT  
 <213> Conus laterculatus

<400> 160  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

09910082 0300T660



Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp  
35 40 45

Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys  
50 55 60

Asn Val Ser Arg Ser Lys Cys Asn  
65 70

<210> 161

<211> 27

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
Tr

<400> 161

Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn  
20 25

<210> 162

<211> 363

<212> DNA

<213> Conus laterculatus

<400> 162

acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgcctcg 120

aggtcgacca ccaatctctc catgctgact cggaagtgtc ggccttcogg aagctattgt 180

cgtgcgaata gtaaatgctg cagtggatgc gatcggaaca gaagtaaag taactagctg 240

attggcgctc taaacttcct ccttctgcct gagtcctcca tacctgagag tggatcatgaa 300

ccactcatca cctactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360

tgc 363

<210> 163

<211> 72

<212> PRT

<213> Conus laterculatus

<400> 163

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
35 40 45

0910033-07301  
T02340-23007660

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys  
50 55 60

Asp Arg Asn Arg Ser Lys Cys Asn  
65 70

<210> 164

<211> 27

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
r, O-sulpho-Tyr or O-phospho-Ty

<400> 164

Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys  
1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn  
20 25

<210> 165

<211> 391

<212> DNA

<213> Conus leopardus

<220>

<221> misc\_feature

<222> (1)..(391)

<223> n may be any nucleotide

<400> 165

atgaaactga cgtgtgtggt gatcgtagct gtgctgttcc tgacggcctg tcaactcact 60

acagctgaca tctccagagg tacgcggaag cgtcgtgctc tgaggtcgac caccaaactc 120

tccaggtcgc tctttgagtg cgcgccttcc ggtggacgtt gtggtttttt aaagtcctgc 180

tgccaaggat attgcgatgg gaaagcact tcatgtgtga gtggcccata cagcatctga 240

tcttcccgcc ttcagtgtc tatccttttc tgctgagtc ctccatacct ctgagcggtc 300

atgaaccact caacacctac tcctctggag gcttcaggga actatattaa aataaagccg 360

cattgcaacg aaanaaaaaa aaaaaaaaaa a 391

<210> 166

<211> 79

<212> PRT

<213> Conus leopardus

<400> 166

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala  
35 40 45

09910082-072301

Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr  
50 55 60

Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile  
65 70 75

<210> 167  
<211> 37  
<212> PRT  
<213> Conus leopardus

<220>  
<221> PEPTIDE  
<222> (1)..(37)  
<223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy Glu; Xaa at r  
esidue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35 is Tyr,  
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
Y

<400> 167  
Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys  
1 5 10 15

Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser  
20 25 30

Gly Xaa Xaa Ser Ile  
35

<210> 168  
<211> 365  
<212> DNA  
<213> Conus leopardus

<400> 168  
atgaaactga cgtgtgtggt gatcgctcgct gtgctgttcc tgacggcctg tcaactcact 60  
acagctgaca tctccagagg tacgtggaag catcgtggtg tggggtcgac caccggactc 120  
tccccgtggc ccttggaactg cacggctccc agtcaacctt gtggttatatt tcttaggtgc 180  
tgtggacatt gcgatgtacg cagggtatgt acgagtggct gatccggcgt ctgatctttc 240  
cgctttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggcatgaac 300  
cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg 360  
caatg 365

<210> 169  
<211> 73  
<212> PRT  
<213> Conus leopardus

<400> 169  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg  
20 25 30

Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr  
35 40 45

09910082-072301  
T02210-2800T660

Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys  
50 55 60

Asp Val Arg Arg Val Cys Thr Ser Gly  
65 70

<210> 170  
<211> 30  
<212> PRT  
<213> Conus leopardus

<220>  
<221> PEPTIDE  
<222> (1)..(30)  
<223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is  
Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-  
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 170  
Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa  
1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser  
20 25 30

<210> 171  
<211> 381  
<212> DNA  
<213> Conus leopardus

<400> 171  
atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60  
acagctgaca tctccagagg tacgcggaag catcgtgctc tgaggtcgac caccaaactc 120  
tccaggctgc cctctagggtg catgtctccc ggtggaattt gtggtgattt tgggtgactgc 180  
tgcgaaattt gcaatgtgta cggatatatgt gtgagtgact tacccgcat ctgatctttc 240  
cgccttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggcatggac 300  
cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg 360  
caaaaaaaaa aaaaaaaaaa a 381

<210> 172  
<211> 77  
<212> PRT  
<213> Conus leopardus

<400> 172  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met  
35 40 45

Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys  
50 55 60

Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile  
65 70 75

09910003 09910004

<210> 173  
 <211> 31  
 <212> PRT  
 <213> Conus leopardus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 173  
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa  
 1 5 10 15  
 Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile  
 20 25 30

<210> 174  
 <211> 404  
 <212> DNA  
 <213> Conus leopardus

<400> 174  
 atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60  
 acagctgatg attccagagg tacacggaag catcgtgctc tgaggtcaac caccaaactc 120  
 tccaggtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc 180  
 tgcggatatt gcgaaacgtt ttacaatacg tgtagatgag ttggctgac cggcgcttga 240  
 tttttccgcc ttctgttgct ctatcttttt ctgcctgagt cctcccatac ccggttgagt 300  
 ggtccatgaa ccaactccaac acctactccc tccttggaag cttccaaag aaacgacatt 360  
 taaaataaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 404

<210> 175  
 <211> 72  
 <212> PRT  
 <213> Conus leopardus

<400> 175  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala  
 35 40 45  
 Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys  
 50 55 60  
 Glu Thr Phe Tyr Asn Thr Cys Arg  
 65 70

<210> 176  
 <211> 27  
 <212> PRT  
 <213> Conus leopardus

09910082 072201

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 176  
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys  
 1 5 10 15

Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg  
 20 25

<210> 177  
 <211> 292  
 <212> DNA  
 <213> Conus lynceus

<400> 177  
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagacg tacacagaag catcgtgccc tgaggtcgac caccaatctc 120  
 tccatgtcga ctgctgcaa gtctccogga tcaccatgta gtgtgacatc gtataactgc 180  
 tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac 240  
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg 292

<210> 178  
 <211> 75  
 <212> PRT  
 <213> Conus lynceus

<400> 178  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser  
 35 40 45  
 Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys  
 50 55 60  
 Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu  
 65 70 75

<210> 179  
 <211> 30  
 <212> PRT  
 <213> Conus lynceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 179

0091008.0334

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys  
1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu  
20 25 30

<210> 180  
<211> 355  
<212> DNA  
<213> Conus lynceus

<400> 180  
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60  
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggctgac caccaaacta 120  
tccatgtata ctgctgctgc aggtccagga gcaatttgtc ctaatagggt atgctgctgt 180  
tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc ccccttctgt 240  
gctctatcct ttttctgcct gagtcctcca tacctgagaa tggatcatgaa ccaactcatca 300  
cctactcctc ttggagacct cagaggagct aactgaaat aaaagccgca ttggc 355

<210> 181  
<211> 74  
<212> PRT  
<213> Conus lynceus

<400> 181  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30  
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly  
35 40 45  
Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys  
50 55 60  
Arg Thr His Leu Cys His Ser Arg Thr Gly  
65 70

<210> 182  
<211> 28  
<212> PRT  
<213> Conus lynceus

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182  
Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa  
1 5 10 15  
Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
20 25

0910082 07301

<400> 186



atgaaactga cgtgtgtggt gatcgtcgcc gagctactcc taacggcctg tcaactcatc 60  
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgac caccaatctc 120  
tccatgctga ctcggaagtg ctggtctccc ggaacctatt gtcgtgcgca tagtaaatgc 180  
tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc 240  
ctccttctgt gctctatcct ttttctgcct ggtcctcca taactgagaa tggatcatgaa 300  
ccactcatca cctactcctc tggaggcctc agaggagcct aactgaaat aaaagccgca 360  
ttgg 364

<210> 187  
<211> 72  
<212> PRT  
<213> Conus lynceus

<400> 187  
Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30  
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
35 40 45  
Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys  
50 55 60  
Asp Gln Asn Arg Asn Lys Cys Tyr  
65 70

<210> 188  
<211> 27  
<212> PRT  
<213> Conus lynceus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 5 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 188  
Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys Cys  
1 5 10 15  
Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa  
20 25

<210> 189  
<211> 318  
<212> DNA  
<213> Conus magus

<400> 189  
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
acggcctgtc aactcatcac agctgatgac tcagaggta cgcagaagca tcgtgccctg 120  
aggtcggaca ccaaactctc catgtcgact cgctgcaagg gtacaggaaa accatgcagt 180

aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgtgg ctgatccagt 240  
gcctgatctt ccccttctg tgctctatcc tttttctgcc tgagtcctcc ttacctgaga 300  
gtggtcatga accactca 318

<210> 190  
<211> 71  
<212> PRT  
<213> Conus magus

<400> 190  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30  
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45  
Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
50 55 60  
Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 191  
<211> 25  
<212> PRT  
<213> Conus magus  
<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 191  
Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15  
Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 192  
<211> 259  
<212> DNA  
<213> Conus magus

<400> 192  
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtgcgcgt gctgctctg 60  
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgcctg 120  
aagtcggaca ccaaactctc catgttaact ttgcgctgcg catcttaagg aaaaccttgt 180  
ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg 240  
atccggcgtc tgatcttcc 259

<210> 193  
<211> 72  
<212> PRT

<213> Conus magus

<400> 193

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
65 70

<210> 194

<211> 26

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
spho-Ty

<400> 194

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 195

<211> 254

<212> DNA

<213> Conus magus

<400> 195

gaattttcag catcaccaaaa accatcatca aaatgaaact gacgtgtgtg gtgatcgctcg 60

ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120

agcatcgctgc cctgaggtcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag 180

gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaat 240

ttggctgata cgcc 254

<210> 196

<211> 71

<212> PRT

<213> Conus magus

<400> 196

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
50 55 60

Cys Asn Arg Gly Lys Phe Gly  
65 70

<210> 197

<211> 25

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 197

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
20 25

<210> 198

<211> 358

<212> DNA

<213> Conus miles

<400> 198

ggatccatga aactgacgtg cgtggtgatc atcgccatgc tgttcctgac agcctatcaa	60
ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcgtgctct gaggccagct	120
gacaaacacc tcaggttgac caagcgttgc aatgatcgcg gtggagggtg cagtcaacat	180
cctcactgct gcggtggaac ttgcaataag cttattggcg tatgtctgta aagctgggtct	240
gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcac catacctgtg	300
aatggttaag agccactcaa tacctattcc tctgggggct tcagaggaac tactttac	358

<210> 199

<211> 74

<212> PRT

<213> Conus miles

<400> 199

Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala  
1 5 10 15

Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His  
20 25 30

Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys  
35 40 45

Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly  
50 55 60

Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
65 70

001003 02301660

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<210> 203
<211> 25
<212> PRT
<213> Conus monachus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
sulpho-Tyr or O-phospho-Ty

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<211> 258

<212> DNA

<213> Conus obscurus

<400> 207

```
ctctctctct ctctgctgga caggctgcct ccctgcatga aaggcggatc gtcatgccgc      60
gggtactacgg gagtctgttg cggtttttgc agtgatttcg gctataaatg tagggactat      120
ccccaaaact gatcttcccc cttctgtgct ctatcctttt ctgtccgagt cctcctgacc      180
tgagagtggg catgaaccac tcatcaccta cccctctggg gcttcacagg atctacattg      240
aaataaaagc cgcattgc                                         258
```

<210> 208

<211> 39

<212> PRT

<213> Conus obscurus

<400> 208

```
Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg
1          5          10          15
Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
          20          25          30
Cys Arg Asp Tyr Pro Gln Asn
          35
```

<210> 209

<211> 35

<212> PRT

<213> Conus obscurus

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 209

```
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1          5          10          15
Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa
          20          25          30
Xaa Gln Asn
          35
```

<210> 210

<211> 259

<212> DNA

<213> Conus obscurus

<400> 210

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ctctctctct ctctgctgga caggctgcact cgtctgttgc ctgacggaac gtcttgccct      60
tttagtagga tcagatgctg cgggtacttgc agttcaatct taaagtcatg tgtgagctga      120
tccagcgggt gatcttcctc cctctgtgct ccatacctttt ctgcctgagt tctccttacc      180
tgagagtggg catgaaccac tcatcaccta ctcttctgga ggcttcagag gagctacatt      240
```

259

<400> 211  
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg  
1 5 10 15

```
<220>
<221>  PEPTIDE
<222>  (1)..(28)
<223>  Xaa at residue 3 is Pro or Hyp
```

```
<400> 212
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1          5          10          15
```

```
<210> 213
<211> 330
<212> DNA
<213> Conus pulicarius
```

```
<220>
<221> misc_feature
<222> (1)..(330)
<223> n may be any nucleotide
```

[illegible]

```
<210> 214
<211> 76
<212> PRT
<213> Conus pulicarius
```

```

<400> 214
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1      5      10      15
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His
      20      25      30

```



Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
35 40 45

Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
50 55 60

Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
65 70 75

<210> 215  
<211> 30  
<212> PRT  
<213> Conus pulicarius

<220>  
<221> PEPTIDE  
<222> (1)..(30)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H  
yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
r, O-sulpho-Tyr or O-phospho-Ty

<400> 215  
Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
20 25 30

<210> 216  
<211> 282  
<212> DNA  
<213> Conus purpurascens

<400> 216  
atgaaactga cgtgtgtggt gatcgctgcc gtgctgttcc tgacggcctg tcaactcatc 60  
acagctgatg actccagacg tacgcagaag catcgtgcc tgaggtcgac caccaaaggc 120  
gccacgtcga atcgcccctg caagacaccc ggacgaaaat gttttccgca tcagaaggac 180  
tgctgoggte gagcgtgcat catcacaata tgccctgat cttccccctt ctgtgctgta 240  
tccttttctg cctgagtctc cttacctgag agtggtcatg aa 282

<210> 217  
<211> 72  
<212> PRT  
<213> Conus purpurascens

<400> 217  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys  
35 40 45

Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg  
50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro  
65 70

00010082 02201

<210> 218  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1, 5, 11 and 27 is Pro or Hyp

<400> 218  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15  
 Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
 20 25

<210> 219  
 <211> 340  
 <212> DNA  
 <213> Conus purpurascens

<400> 219  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccggagc atattgtaat 180  
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240  
 gcctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct tacctaagag 300  
 tggatcatgaa ccaactcatca ccttctcctc tggaggettc 340

<210> 220  
 <211> 71  
 <212> PRT  
 <213> Conus purpurascens

<400> 220  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu  
 35 40 45  
 Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys  
 50 55 60  
 Lys Val Gly Gly Thr Cys Gly  
 65 70

<210> 221  
 <211> 26  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE

Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
20 25

<210> 225  
<211> 328  
<212> DNA  
<213> Conus radiatus

<400> 225  
gctgatgcct gatcttcacg gttcttccct gtctcctttg gcatcaccaa aaccatcatc 60  
aaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 120  
atcacagctg atgactccag aggtatgcag aaacatcatg ccctggggtc gatcagcagt 180  
ctctttaagt cgaccogtca tggctgcaaa cccctcaaac gtcgttgttt caatgataaa 240  
gaatgctgca gcaaattttg caattcagtc cgaaagcagt gtggataaat ggctaaaaaa 300  
ctgaataaaa gccgcattgc aaaaaaaa 328

<210> 226  
<211> 74  
<212> PRT  
<213> Conus radiatus

<400> 226  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
20 25 30  
Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys  
35 40 45  
Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys  
50 55 60  
Phe Cys Asn Ser Val Arg Lys Gln Cys Gly  
65 70

<210> 227  
<211> 28  
<212> PRT  
<213> Conus radiatus

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i  
s Pro or Hy

<400> 227  
His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys  
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
20 25

<210> 228  
<211> 250  
<212> DNA  
<213> Conus radiatus

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```
<210> 229
<211> 74
<212> PRT
<213> Conus radiatus
```

```

<210> 230
<211> 28
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
s Pro or Hy

```

<210>	231
<211>	435
<212>	DNA
<213>	Conus radiatus

[illegible]

cccccttctgt gctctatcct tttctgccc gagtcccca tacctgagag tagtcatgaa 360  
 ccactgatta cctactcctc tggagggcct cagaggagct actttgaaat aaaagcccgc 420  
 attgcaaaaa aaaaa 435

<210> 232  
 <211> 72  
 <212> PRT  
 <213> Conus radiatus

<400> 232  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
 20 25 30

Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro  
 35 40 45

Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys  
 50 55 60

Lys Ser Tyr Asn Lys Lys Cys Gly  
 65 70

<210> 233  
 <211> 27  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-  
 phospho-Ty

<400> 233  
 Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys  
 1 5 10 15

Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly  
 20 25

<210> 234  
 <211> 392  
 <212> DNA  
 <213> Conus rattus

<400> 234  
 ggatccatga aactgacgtg catggtgatc atcgccgtgc tgttctgac agcctgtcaa 60  
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct 120  
 gacaaacaca tcaggttgac caagcgttgc aatgctcgca atgatggttg cagtcaacat 180  
 tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct 240  
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac catacctgtg 300  
 aatgggtaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360

05910082.02391

aaagccacat tgcaaaaaaa aaaaaaaaaa aa

392

<210> 235

<211> 74

<212> PRT

<213> Conus rattus

<400> 235

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys  
35 40 45

Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly  
50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
65 70

<210> 236

<211> 27

<212> PRT

<213> Conus rattus

<400> 236

Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 237

<211> 395

<212> DNA

<213> Conus rattus

<400> 237

ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttctctgac agcctgtcaa 60

ctcgatgcag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120

gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180

cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctgggtct 240

gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac catacctgtg 300

aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360

aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395

<210> 238

<211> 74

<212> PRT

<213> Conus rattus

<400> 238

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro

09910082-07201

20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
65 70

<210> 239  
<211> 27  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 12 is Pro or Hyp

<400> 239  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 240  
<211> 390  
<212> DNA  
<213> Conus rattus

<400> 240  
ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60  
ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120  
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtgggtg cagtcaacat 180  
cctcaatgct gcagtggtgc ttgcaataag actttgggcg tatgtctgta aagctggtct 240  
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcac caccctgtg 300  
aatgggtaag agccactcaa tacctactcc tctggggggt tcagaggaac tacattaaat 360  
aaagccacat tgaaaaaaaaaaaaaaaaaaaaa 390

<210> 241  
<211> 74  
<212> PRT  
<213> Conus rattus

<400> 241  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
50 55 60

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Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
65 70

<210> 242  
<211> 27  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 12 is Pro or Hyp

<400> 242  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
20 25

<210> 243  
<211> 379  
<212> DNA  
<213> Conus stercusmuscarum

<400> 243  
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcttg 60  
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccttg 120  
aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180  
aggcttatgt atgactgctg cagcggttct tgcagcggct acacaggtag atgtggctga 240  
tccagcgct gatcttcccc cttctgtgct ctatcctttt ctgcctgggt cctccttacc 300  
tgagagtggg catgaaccac tcatcaccta ctctcttgga ggcctcagag gagttacaat 360  
gaaataaaag ccgcattgc 379

<210> 244  
<211> 73  
<212> PRT  
<213> Conus stercusmuscarum

<400> 244  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser  
35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser  
50 55 60

Cys Ser Gly Tyr Thr Gly Arg Cys Gly  
65 70

<210> 245  
<211> 27  
<212> PRT

0910082.07301

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 245

Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys  
20 25

<210> 246

<211> 35

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 246

Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg  
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa  
20 25 30

Xaa Ser Asn  
35

<210> 247

<211> 380

<212> DNA

<213> Conus stercusmuscarum

<400> 247

accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120

aggtcgaaga ccaaactctc catgttaact ttgcgctgcy catcttacgg aaaaccttgt 180

ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgtagctg 240

atccggcgtc tgatcttccc ccttctgtgc totatccttt tctgcctgag tcctccttac 300

ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggctcaga ggagctacaa 360

tgaaataaaa gccgcattgc 380

<210> 248

<211> 72

<212> PRT

<213> Conus stercusmuscarum

<400> 248

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15

09910082-072701

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn  
65 70 75

<210> 255  
 <211> 36  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 255  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn  
 20 25 30

Xaa Xaa Lys Asn  
 35

<210> 256  
 <211> 233  
 <212> DNA  
 <213> Conus striatus

<400> 256  
 gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60  
 cgggttcttgcc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc ccccttcttg 120  
 tgctctatcc ttttctgcct gggctctcct tacctgagag tggatcatgaa ccaactcatca 180  
 cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcgc tgc 233

<210> 257  
 <211> 30  
 <212> PRT  
 <213> Conus striatus

<400> 257  
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr  
 1 5 10 15

Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly  
 20 25 30

<210> 258  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 258  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys  
 20 25

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<210> 259  
 <211> 310  
 <212> DNA  
 <213> Conus striatus

<400> 259  
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaattgcg ctgatccagc 240  
 gctgatctt ccccttctg tgctctatcc tttctgctg agtcctctta cctgagagtg 300  
 gtcatgaacc 310

<210> 260  
 <211> 71  
 <212> PRT  
 <213> Conus striatus

<400> 260

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala  
 35 40 45

Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 261  
 <211> 25  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 261  
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 262  
 <211> 256  
 <212> DNA  
 <213> Conus striatus

<400> 262

09910082-072301

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
 aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt 180  
 ggtattttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgtagctg 240  
 atccggcgctc tgatct 256

<210> 263  
 <211> 72  
 <212> PRT  
 <213> Conus striatus

<400> 263  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30  
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu  
 35 40 45  
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys  
 50 55 60  
 Asp Pro Ala Lys Lys Thr Cys Thr  
 65 70

<210> 264  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa at residue 7 and  
 d 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mon  
 o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 264  
 Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr  
 20 25

<210> 265  
 <211> 229  
 <212> DNA  
 <213> Conus striatus

<400> 265  
 tctaggctcct ccggcagccc ctgtggtggt actagtatat gctgtggtag atgctatagg 60  
 ggtaaatgta cgtagctcat cgggcgtctg atcttccccc ttctgtgctc catccttttc 120  
 tgcctgagtc ctccttacct gagagtgggc gtgaaccact catcgctac tcctctggag 180  
 gcttcagagg ggctacacta aaataaaaagc tatattgcaa tgaaaaaaa 229

<210> 266  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<400> 266  
 Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Tyr Arg Gly Lys Cys Thr  
 20

<210> 267  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 267  
 Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Xaa Arg Gly Lys Cys Thr  
 20

<210> 268  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 268  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys  
 20 25

<210> 269  
 <211> 292  
 <212> DNA  
 <213> Conus striolatus

<400> 269  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgtctt gctgctcctg 60  
 acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120  
 aggtcgacta ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt 180  
 aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc 240  
 gtctgatctt ccccttctg tgctctatcc tttttctgctt gagtctcct ta 292



<210> 270  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 270  
 Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Leu Thr Thr  
 1 5 10 15  
 Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45  
 Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60  
 Cys Asn Arg Gly Arg Cys Gly  
 65 70

<210> 271  
 <211> 25  
 <212> PRT  
 <213> Conus striolatus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
 -sulpho-Tyr or O-phospho-Ty

<400> 271  
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 272  
 <211> 259  
 <212> DNA  
 <213> Conus striolatus

<400> 272  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgctgacg 60  
 gcgtgtcaac tcatcacagc tgaggactcc agaggtacac agaagcatcg taccctgagg 120  
 tcgaccgtca gacgctccaa gtccgagttg actacgagat gcaggccttc aggatccaac 180  
 tgttgtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc 240  
 gggcgtctga tctttcccc 259

<210> 273  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 273  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys  
 1 5 10 15  
 Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr

09910082.072301

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<210> 274
<211> 24
<212> PRT
<213> Conus striolatus
```

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<220>
<221>  PEPTIDE
<222>  (1)..(24)
<223>  Xaa at residue 3 is Pro or Hyp
```

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<400> 274
Cys Arg Xaa Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
1          5          10          15
Arg Cys Val Asn Arg Arg Cys Thr
          20

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<210> 275
<211> 280
<212> DNA
<213> Conus striolatus
```

<400>	275								
acccaaacc	tcatcaaat	gaaactgacg	tgtgtggatga	togtgcogct	tctgttcctg				60
acggcgtgtc	aactcatcac	agctgaggac	tccagaggta	cacagaagca	togttccctg				120
aggtcgacta	ccaaagtctc	caagtcgact	agctgcatga	aagccgggtc	ttattgcgtc				180
gctactacga	gaatctgctg	cggttattgc	gcttatttcg	gcaaaaatatg	tattgactat				240
ccccaaaaact	gatcttcccc	ctactgtgct	ctatcctttt						280

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<210> 276
<211> 77
<212> PRT
<213> Conus striolatus
```

```

<400> 276
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1          5          10          15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg
 20          25          30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35          40          45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
 50          55          60

Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn
 65          70          75

```





<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 is Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 284  
 Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg  
 20 25

<210> 285  
 <211> 379  
 <212> DNA  
 <213> Conus tulipa

<400> 285  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctctg 60  
 acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccctg 120  
 gggtcgacca ccaaactcac cttgtcgact cgctgcttgt caccocggatc ttcattgttca 180  
 ccgactagtt ataattgctg caggtcttgc aatccataca gcagaaaatg taggggctaa 240  
 tccagcgct gatcttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300  
 tgaaagtggg catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360  
 gaaataaaaag ccgcattgc 379

<210> 286  
 <211> 73  
 <212> PRT  
 <213> Conus tulipa

<400> 286  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Ser Arg Lys Cys Arg Gly  
 65 70

<210> 287  
 <211> 27  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and

09010087.072301

<400> 287

Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg  
20 25

<211> 401

<212> DNA

<213> Conus viola

accaaaaacca tcatacaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120

aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag 180

gttccgaatc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa 240

gaatggtaaa tctggctgat ccagcgcttg atcttcccc ttctgactgt ctccgacctt 300

ttctgcctga gtcctcctta cctgagaggt gtcatgaacc actcatcacc tactcccctg 360

gaagcttcag aggaqctaca ttgaaataaa agccgcattg c 401

<210> 289

<211> 76

<212> PRT

<213> Conus viola

<400> 289

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr  
35 40 45

Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys  
50 55 60

Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
65 70 75

<210> 290

<211> 31

&lt;212&gt; PRT

<213> Conus viola

 $\langle 220 \rangle$ 

<221> PEPTIDE

<222> (1) .. (31)

<223> Xaa at residue 29 and 30 is Glu or gamma-carboxy Glu; Xaa at residue 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo Trp

<400> 290

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg

1                      5                      10                      15  
 Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa  
                  20                      25                      30

<210> 291  
 <211> 372  
 <212> DNA  
 <213> Conus viola

<400> 291  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattat agctggggac tccagaggta cgcagttgca tcgtgccctg 120  
 aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtagaggatc atcatgtcgt 180  
 aggacttcgt atgactgctg cacgggttct tgcagaaatg gtaaattgtg ctgatccagc 240  
 gcctgatctt ccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300  
 tgggcatgaa ccactcatca cctactccct ggaagcttca gaggagctac attgaaataa 360  
 aagccgcatt gc 372

<210> 292  
 <211> 71  
 <212> PRT  
 <213> Conus viola

<400> 292  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1                      5                      10                      15  
 Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg  
                  20                      25                      30  
 Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser  
                  35                      40                      45  
 Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
                  50                      55                      60  
 Cys Arg Asn Gly Lys Cys Gly  
 65                      70

<210> 293  
 <211> 25  
 <212> PRT  
 <213> Conus viola  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O  
                  -sulpho-Tyr or O-phospho-Ty

<400> 293  
 Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys  
 1                      5                      10                      15  
 Thr Gly Ser Cys Arg Asn Gly Lys Cys  
                  20                      25

09910082-02201

$\langle 210 \rangle$	297
$\langle 211 \rangle$	373





acggcctgtc aattcatcac agctgatgac tccagaagta cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaaacactt tatgttgact tgggtactgca cgccttatgg aggacattgt 180  
 gggtattata atgactgctg cagtcacaa tgcaatataa acagaaataa atgtgagtag 240  
 ctgatccggc atctgatctg tgctcgccct aacctgagag tggatcatgaa ccactcatca 300  
 tctactcttc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 353

<210> 301  
 <211> 73  
 <212> PRT  
 <213> Conus viola

<400> 301  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr  
 35 40 45  
 Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60  
 Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 65 70

<210> 302  
 <211> 28  
 <212> PRT  
 <213> Conus viola

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is  
 s Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mo  
 no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 302  
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 303  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 303  
 ggatccatga aactgacgtg cgtgggtgatt atcgccgtgc tgttcctgac ggctgtcaa 60  
 ctcatcag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120  
 gacaaaaact ccaagttgac caggggaatgc acacctccag atggagcttg tggtttacct 180  
 acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240

tcccccttctg tgctctatcc tctttggcct gagtcaccca tacctgtgct cgag

294

<210> 304  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 304  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
 20 25 30  
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys  
 35 40 45  
 Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
 50 55 60  
 Cys Asp Met Ala Asn Asn Arg Cys Leu  
 65 70

<210> 305  
 <211> 27  
 <212> PRT  
 <213> Conus pulicarius  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
 and 12 is Pro or Hy

<400> 305  
 Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
 1 5 10 15  
 Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

<210> 306  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 306  
 ggatccatga aactgacgtg cgtgggtgatt atcgccgtgc tgttcctgac ggctgtcaa 60  
 ctcatcag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120  
 gacaaaaact cccagttgac cagggaatgc acacctccag gtggagcttg tggtttacct 180  
 acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaaag cgtctgatat 240  
 tcccccttctg tgctctatcc tctttggcct gagtcaccca tacctgtgct cgag 294

<210> 307  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 307  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

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Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe

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50              55              60
Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His
65              70              75              80

<210> 311
<211> 34
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residue 5 and 29 is Glu or gamma-carboxy Glu; Xaa at resid
ue 4 and 31 is Pro or Hyp; Xaa at residue 27 is Tyr, 125I-Tyr, mo
no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 311
Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
1              5              10              15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser
20              25              30

Leu His

<210> 312
<211> 342
<212> DNA
<213> Conus stercusmuscarum

<220>
<221> misc_feature
<222> (1)..(342)
<223> n may be any nucleotide

<400> 312
agatccatga aactgacgtg cgtgggtgatc gtcgccgtgc tgctcctgac ggctgtgtcaa
60
ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtgggacacc
120
aaactcccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat
180
gactgtgtgca gcggttctctg caccagaggt agatgtggct gatccagcgc ctgatcttcc
240
cccttctgtg ctctatcctt ttctgcttga gtcatcatac ctgtgctcga gcgttactag
300
tggatccgag ctcggtaacca agcttggcgt aatcataaaa nc
342

<210> 313
<211> 71
<212> PRT
<213> Conus stercusmuscarum

<400> 313
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1              5              10              15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
20              25              30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly
35              40              45

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Pro

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<400>   318
Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1                               5 10 15
Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
                20 25 30

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```
<210> 319
<211> 27
<212> PRT
<213> Conus arenatus
```

```
<210> 320
<211> 28
<212> PRT
<213> Conus arenatus
```

```
<210> 321
<211> 30
<212> PRT
<213> Conus arenatus
```

```
<210> 322
<211> 30
<212> PRT
<213> Conus arenatus
```

```

<400> 322
Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
1      5      10      15
Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr
      20      25      30

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<210>	328
<211>	31



<212> PRT  
 <213> Conus bullatus

<400> 328  
 Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15  
 Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
 20 25 30

<210> 329  
 <211> 26  
 <212> PRT  
 <213> Conus bullatus

<400> 329  
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr  
 20 25

<210> 330  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 330  
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Lys Tyr Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 331  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<400> 331  
 Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15  
 Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys  
 20 25 30

Lys Pro Asn Asn  
 35

<210> 332  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 332  
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Asn Gly Arg Cys  
 20 25

<210> 333  
 <211> 25  
 <212> PRT

0910082.072301

<213> Conus catus

<400> 333

Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys  
20 25

<210> 334

<211> 25

<212> PRT

<213> Conus catus

<400> 334

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
20 25

<210> 335

<211> 28

<212> PRT

<213> Conus catus

<400> 335

Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
20 25

<210> 336

<211> 25

<212> PRT

<213> Conus catus

<400> 336

Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 337

<211> 26

<212> PRT

<213> Conus catus

<400> 337

Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 338

<211> 25

<212> PRT

<213> Conus catus

<400> 338

Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys  
1 5 10 15

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Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 339  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<400> 339  
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr  
20 25 30

Pro

<210> 340  
<211> 26  
<212> PRT  
<213> Conus consors

<400> 340  
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 341  
<211> 25  
<212> PRT  
<213> Conus consors

<400> 341  
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 342  
<211> 36  
<212> PRT  
<213> Conus consors

<400> 342  
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met  
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn  
20 25 30

Tyr Pro Gln Asn  
35

<210> 343  
<211> 27  
<212> PRT  
<213> Conus catus

<400> 343  
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys

09910082-072301

1                    5                    10                    15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
20                    25

<210> 344

<211> 25

<212> PRT

<213> Conus consors

<400> 344

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
1                    5                    10                    15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
20                    25

<210> 345

<211> 26

<212> PRT

<213> Conus consors

<400> 345

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
1                    5                    10                    15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20                    25

<210> 346

<211> 25

<212> PRT

<213> Conus consors

<400> 346

Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys  
1                    5                    10                    15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20                    25

<210> 347

<211> 35

<212> PRT

<213> Conus consors

<400> 347

Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1                    5                    10                    15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe  
20                    25                    30

Pro Ser Asn  
35

<210> 348

<211> 25

<212> PRT

<213> Conus circumcisis

<400> 348

Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
1                    5                    10                    15

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Ser Gly Ser Cys Ser Asn Gly Arg Cys  
20 25

<210> 349  
<211> 35  
<212> PRT  
<213> Conus circumciscus

<400> 349  
Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1 5 10 15  
Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe  
20 25 30

Pro Ser Asn  
35

<210> 350  
<211> 27  
<212> PRT  
<213> Conus circumciscus

<400> 350  
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys  
20 25

<210> 351  
<211> 35  
<212> PRT  
<213> Conus circumciscus

<400> 351  
Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1 5 10 15  
Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr  
20 25 30

Pro Ser Asn  
35

<210> 352  
<211> 28  
<212> PRT  
<213> Conus dalli

<400> 352  
Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys  
1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu  
20 25

<210> 353  
<211> 25  
<212> PRT  
<213> Conus distans

<220>  
<221> PEPTIDE

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<222> (1)..(25)

<223> Xaa is Hyp

<400> 353

Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly  
1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala  
20 25

<210> 354

<211> 27

<212> PRT

<213> Conus ermineus

<400> 354

Pro Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys  
1 5 10 15

Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro  
20 25

<210> 355

<211> 27

<212> PRT

<213> Conus ermineus

<400> 355

Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys  
1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
20 25

<210> 356

<211> 27

<212> PRT

<213> Conus geographus

<400> 356

Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys  
1 5 10 15

Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr  
20 25

<210> 357

<211> 29

<212> PRT

<213> Conus geographus

<400> 357

Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys  
1 5 10 15

Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr  
20 25

<210> 358

<211> 30

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species







Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys  
1 5 10 15

<213> Conus laterculatus

Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
1 5 10 15

<213> Conus laterculatus

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys  
1 5 10 15

<213> Conus leopardus

Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys  
1 5 10 15

Gly Pro Tyr Ser Ile  
35

<213> Conus leopardus

Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro  
1 5 10 15

<213> Conus leopardus

Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu



<210> 379  
 <211> 25  
 <212> PRT  
 <213> Conus monachus

<400> 379  
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

<210> 380  
 <211> 35  
 <212> PRT  
 <213> Conus obscurus

<400> 380  
 Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly  
 1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr  
 20 25 30

Pro Gln Asn  
 35

<210> 381  
 <211> 28  
 <212> PRT  
 <213> Conus obscurus

<400> 381  
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25

<210> 382  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is Hyp

<400> 382  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro  
 20 25

<210> 383  
 <211> 26  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

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Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
20 25

<210> 389  
<211> 28  
<212> PRT  
<213> Conus radiatus

<400> 389  
Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys  
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys  
20 25

<210> 390  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 390  
Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 391  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 391  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
20 25

<210> 392  
<211> 27  
<212> PRT  
<213> Conus rattus

<400> 392  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
20 25

<210> 393  
<211> 34  
<212> PRT  
<213> Conus rattus

<400> 393  
Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys  
1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser  
20 25 30

Leu His

<400> 394

Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys  
20 25

$$\begin{array}{ll} \langle 210 \rangle & 404 \\ \langle 211 \rangle & 24 \end{array}$$

<212> PRT  
 <213> Conus striolatus

<400> 404  
 Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Val Asn Arg Arg Cys Thr  
 20

<210> 405  
 <211> 35  
 <212> PRT  
 <213> Conus striolatus

<400> 405  
 Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg  
 1 5 10 15  
 Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr  
 20 25 30

Pro Lys Asn  
 35

<210> 406  
 <211> 28  
 <212> PRT  
 <213> Conus textile

<400> 406  
 Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

<210> 407  
 <211> 31  
 <212> PRT  
 <213> Conus viola

<400> 407  
 Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15  
 Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
 20 25 30

<210> 408  
 <211> 25  
 <212> PRT  
 <213> Conus viola

<400> 408  
 Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 409  
 <211> 36  
 <212> PRT  
 <213> Conus viola



&lt;400&gt; 409

Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn  
 20 25 30

Asn Pro Asn Asn  
 35

&lt;210&gt; 410

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 410

Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15

Lys Tyr Ser Cys Gly Asn Gly Lys Cys  
 20 25

&lt;210&gt; 411

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 411

Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

&lt;210&gt; 412

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 412

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser  
 1 5 10 15

His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

&lt;210&gt; 413

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 413

Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys  
 1 5 10 15

Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys  
 20 25

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